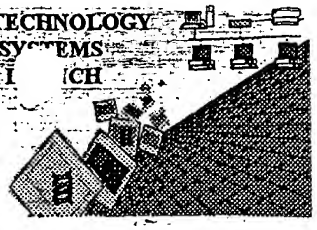

CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/674913 (PCT)

Filing Date: 11-8-00

Date Processed by STIC: 2-5-00

STIC Contact: **Mark Spencer, 703-308-4212**

Nature of Problem:

The CRF (was):

____ (circle one) Damaged or Unreadable (for Unreadable, see attached)

____ Blank (no files on CRF) (see attached)

____ Empty file (filename present, but no bytes in file) (see attached)

____ Virus-infected. Virus name: _____ The STIC will not process the CRF.

____ Not saved in ASCII text

____ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.

____ Did not contain a Sequence Listing. (see attached sample)

✓ Other: Non-compliant sequence format.

PLEASE USE THE CHECKER VERSION 3.0 PROGRAM TO REDUCE ERRORS. SEE BELOW FOR DETAILS:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

Non-compliant sequence listing format. See attached example of correct format and explaination sheet.

COMMON FOR ALL SEQUENCES.
SEQUENCE TYPE: Peptide
SEQUENCE UNIT: Amino Acid
TOPOLOGY: Linear

SEQUENCE ID NO: 1
SEQUENCE LENGTH: 19 amino acids
N V P G H E R M G R G R T S S K E L A
1 5 10 15

SEQUENCE ID NO: 2
SEQUENCE LENGTH: 27 amino acids
R L E A K H R E N V P G H E R M G R G R T S S K E L A
1 5 10 15 20
25

SEQUENCE ID NO: 3
SEQUENCE LENGTH: 17 amino acids
R L E A K H R E N V P G H E R M G
1 5 10 15

SEQUENCE ID NO: 4
SEQUENCE LENGTH: 12 amino acids
M G R G R T S S K E L A
1 5 10

SEQUENCE ID NO: 5
SEQUENCE LENGTH: 15 amino acids

Appendix A To Subpart G to Part 1—Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

<130> 01-00001

<140> US 08/999,999

<141> 1998-02-28

<150> EP 91000000

<151> 1997-12-31

<160> 2

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> Paramecium aurelia

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a Protease from Paramecium sp.

<303> Journal of Fictional Genes

<304> 1

<305> 4

<306> 1 - 7

<307> 1988-06-20

<400> 1

ctactctact ctactctcat ctactatctt ctttggatct ctgagtctgc ctgagtggta 60

ctcttgagtc ctggagatct ctcctctcac atgtgatcgt cgagactgac cgatagatcg 120

ctgactgact ctgagatagt cgagcccgta cgagacccgt cgagggtgac agagagtggg 180

cgcgtgcgcg cagagcgccg cgccggtgcg cgcgcgagtg cgcggtgggc cgcgcgaggg 240

ctttcgcggc agcggcggcg ctttccggcg cgcgcccgtc cgcccctaga cctgagaggt 300

cttctcttcc ctcctcttca ctagagaggt ctatatatac atg gtt tca atg ttc 355

Met Val Ser Met Phe

1 5

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgt ttg ctc 403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

10 15

<210> 2

<211> 18

<212> PRT

<213> Paramecium aurelia

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1 5 10 15

Phe Val

Numeric identifier	Definition	Comments and format	Mandatory (M) or optional (O).
<110>	Applicant	Preferably max. of 10 names; one name per preferable format: Surname, Other Names or Initials.	M.
<120>	Title of Invention		M.
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number.
<140>	Current Application Number.	Specify as: US 07/999,999 or PCT/US96/99999	M, if available.
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available.
<150>	Prior Application Number.	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120.
<151>	Prior Application Filing Date.	Specify as: yyyy-mm-dd	M, if applicable.
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M.
<170>	Software	Name of software used to create the Sequence Listing.	O.
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown.	M.
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues.	M.
<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M.
<213>	Organism	Scientific name, i.e. Genus/ species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence..	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA"
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/ amino acids in feature.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O.
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials.	O.
<302>	Title		O.
<303>	Journal		O.
<304>	Volume		O.
<305>	Issue		O.
<306>	Pages		O.
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy.	O.
<308>	Database Accession Number.	Accession number assigned by database including database name.	O.
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy.	O.
<310>	Patent Document Number.	Document number; for patent-type citations only. Specify as, for example, US 07/999,999.	O.
<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<313>	Relevant Residues	FROM (position) TO (position)	O.
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence.	M.